

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 14:18:50 ; Search time 12.321 Seconds
(without alignments)
888.505 Million cell updates/sec

Title: US-10-757-832-2

Perfect score: 8514
Sequence: 1 MTPPEQAQFALALHAG.....MVETPPICFALGALMNGC 1625

Scoring table:

BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 51470 seqs, 6736768 residues

Total number of hits satisfying chosen parameters: 51470

Minimum DB-seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: /cgm2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 2: /cgm2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 3: /cgm2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 4: /cgm2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 5: /cgm2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep:*
- 6: /cgm2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 7: /cgm2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep:*
- 8: /cgm2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	106	1.2	3690	US-10-995-561-1016	Sequence 1016, Ap
2	103.5	1.2	3714	US-10-995-561-1015	Sequence 1015, Ap
3	103.5	1.2	3717	US-10-821-234-1076	Sequence 1076, Ap
4	101	1.2	1306	US-10-467-657-5406	Sequence 5406, Ap
5	99.5	1.2	2828	US-11-080-991-54	Sequence 54, Appl
6	99.5	1.2	2828	US-11-186-284-49	Sequence 49, Appl
7	99	1.2	1307	US-10-995-561-711	Sequence 711, Ap
8	98	1.2	865	US-10-467-9628-33	Sequence 33, Appl
9	97.5	1.1	7102	US-11-143-980-48	Sequence 48, Appl
10	96	1.1	3655	US-11-075-185-5	Sequence 5, Appl1
11	95.5	1.1	3011	US-10-985-205-3	Sequence 3, Appl1
12	95	1.1	1206	US-10-995-561-709	Sequence 709, Ap
13	95	1.1	2256	US-11-144-368-4	Sequence 4, Appl1
14	95	1.1	5712	US-11-143-980-47	Sequence 47, Appl
15	93.5	1.1	820	US-10-467-657-4910	Sequence 4910, Ap
16	93	1.1	1806	US-10-995-561-812	Sequence 812, App
17	93	1.1	1806	US-10-995-561-915	Sequence 915, App
18	93	1.1	3674	US-11-000-463-454	Sequence 454, App
19	92.5	1.1	557	US-10-821-234-895	Sequence 895, App
20	92.5	1.1	882	US-11-012-762-34	Sequence 34, Appl
21	92	1.1	859	US-10-467-657-8084	Sequence 8084, Ap
22	91.5	1.1	2004	US-10-467-657-84	Sequence 84, Appl
23	91.5	1.1	2004	US-10-467-657-6322	Sequence 6322, Ap
24	91.5	1.1	2059	US-11-087-100-4	Sequence 4, Appl1
25	91.5	1.1	2059	US-11-087-084-4	Sequence 4, Appl1

26	91.5	1.1	2059	US-11-087-085-4	Sequence 4, Appl1
27	91	1.1	423	US-10-793-626-3160	Sequence 3160, Ap
28	91	1.1	440	US-10-525-710-52	Sequence 52, Appl
29	90.5	1.1	468	US-10-467-657-3478	Sequence 3478, Ap
30	90.5	1.1	1304	US-10-821-234-1648	Sequence 1648, Ap
31	90.5	1.1	1572	US-11-143-980-46	Sequence 46, Appl
32	90	1.1	254	US-11-067-323-784	Sequence 784, App
33	90	1.1	3689	US-11-075-185-4	Sequence 4, Appl1
34	89.5	1.1	980	US-11-064-246-10	Sequence 10, Appl
35	89.5	1.1	1560	US-11-059-982-1	Sequence 1, Appl1
36	89.5	1.1	2101	US-10-857-780-23	Sequence 23, Appl
37	89	1.0	254	US-11-067-323-1107	Sequence 1107, Ap
38	89	1.0	530	US-11-055-822-256	Sequence 256, App
39	89	1.0	1432	US-10-510-386-218	Sequence 218, Appl
40	88.5	1.0	617	US-10-878-556A-67	Sequence 67, Appl
41	88.5	1.0	1389	US-10-467-657-334	Sequence 334, App
42	88	1.0	254	US-11-067-323-852	Sequence 852, App
43	87.5	1.0	305	US-11-080-091-2	Sequence 2, Appl1
44	87.5	1.0	519	US-11-080-991-106	Sequence 106, App
45	87	1.0	3063	US-11-186-284-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1					
US-10-995-561-1016					
Sequence 1016, Application US/10995561					
Publication No. US20050272054A1					
GENERAL INFORMATION:					
APPLICANT: CARGILL, Michele et al.					
TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH					
TITLE OF INVENTION: CARDIOVASCULAR DISORDERS AND DRUG RESPONSE, METHODS OF					
TITLE OF INVENTION: DETECTION AND USES THEREOF					
FILE REFERENCE: C001559					
CURRENT APPLICATION NUMBER: US/10/995,561					
CURRENT FILING DATE: 2004-11-24					
NUMBER OF SEQ ID NOS: 85702					
SOFTWARE: FASTSEQ for Windows Version 4.0					
SEQ ID NO 1016					
LENGTH: 3690					
TYPE: PRT					
ORGANISM: Homo sapiens					
US-10-995-561-1016					
Query Match					
Best Local Similarity 18.4%; Pred. No. 11;					
Matches 248; Conservative 155; Mismatches 448; Indels 494; Gaps 65;					
QY	222	IIYALSGVIGRPFKNLASVKNPILNIYVSCMTFSGIVNA-----LIIAELFDI	273		
DB	2264	LIAGTETATLGH-AKTLIAAIVADRTLSEIMSGTGHGLANASPSGEOLRTIAVERLT	2322		
QY	274	FMTPEPVYXWMSIFGEMQAGPFDXALDVPTLLGGIGMAFGIXSTIGKXSTNSAL	333		
DB	2323	LME-----NRADLGAPOAAAEKL	2342		
QY	334	KAAQENGKPAIRYFKQIMAWIPESEDPVPAIISNMEQAIINKECOLENQTAMLR--DRN	391		
DB	2343	AAAGRL-----LAVQEGSLMEWENQ-----ALAYQTRRLAQHNGAGLMDLRAIRAVDAT	2395		
QY	392	AGABFRLSELDSEBOE---VKKIAKCNSTVTTGTNA---LARISSARAAFEKRAAEQT	445		
DB	2396	REAOEINSRQOEIRLORKEIRSDNATLQATLHAARDTLASVFPLLSLDQAKES--	2453		
QY	446	SRVAPVYXWVSGRPGIGKTCFCQNLAKRIASIGDERSVGIIPRAVDVHDVAYGARVVL	505		
DB	2454	-----LERLAASL-----DGARTPL	2468		
QY	506	WDDFGNDVNVKALRIQMLADTCPTVLNCDRIENKGRKX--DSQVITITNQO--TPYPLD	562		
DB	2469	LQWQTFSPAGSKRLRIVEAAEA-----HAQQLGLALNTSIIIDVQDRLTQGAIE	2520		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 14:13:00 / Search time 197.136 Seconds
(without alignments)
3444.190 Million cell updates/sec

Title: US-10-757-832-2

Perfect score: 8514

Sequence: 1 MPPPOBAPGALALHAE.....MVPTPPICFALGALMNNGC 1625

Scoring table:

BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

1: Published Applications_AA_Main:*
2: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US10_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8474	99.5	1625	US-10-757-832-2	Sequence 2, Appl1
2	3572	42.0	1738	US-10-314-739-2	Sequence 2, Appl1
3	343.5	4.0	2179	US-10-224-999A-3481	Sequence 3481, Ap
4	319	3.7	2227	US-09-929-955-12	Sequence 12, Appl
5	319	3.7	2227	US-10-104-966-12	Sequence 12, Appl
6	319	3.7	2227	US-10-719-619-12	Sequence 12, Appl
7	319	3.7	2227	US-10-817-591-12	Sequence 12, Appl
8	309	3.6	2227	US-10-135-988-2	Sequence 2, Appl1
9	304	3.6	2227	US-10-135-988-4	Sequence 4, Appl1
10	302	3.5	2227	US-10-135-988-6	Sequence 6, Appl1
11	190.5	2.2	458	US-10-770-600-53	Sequence 53, Appl
12	177.5	2.1	1285	US-10-424-599-265913	Sequence 265913,
13	177	2.1	652	US-10-472-459-48	Sequence 48, Appl
14	173.5	2.0	516	US-11-051-613-48	Sequence 48, Appl
15	173.5	2.0	516	US-10-352-393-13	Sequence 13, Appl
16	152.5	1.8	627	US-10-222-100-3	Sequence 3, Appl1
17	150	1.8	1133	US-10-156-761-11645	Sequence 11645, A
18	148.5	1.7	512	US-10-352-393-12	Sequence 12, Appl
19	148.5	1.7	7349	US-10-314-657-46	Sequence 46, Appl
20	148.5	1.7	7349	US-10-473-193-46	Sequence 46, Appl
21	142.5	1.7	3816	US-09-808-880-3	Sequence 3, Appl1
22	142.5	1.7	3816	US-10-732-923-20544	Sequence 20544, A
23	140	1.6	2430	US-10-437-963-165599	Sequence 165599,
24	131	1.5	1601	US-10-437-963-195646	Sequence 195646,
25	126.5	1.5	274	US-10-425-115-354307	Sequence 354307,
26	125	1.5	527	US-10-684-129-8	Sequence 8, Appl1
27	124.5	1.5	460	US-10-282-122A-61203	Sequence 61203, A

28	124.5	1.5	1974	4	US-10-369-493-5455	Sequence 5455, Ap
29	124	1.5	3753	3	US-09-980-217-29	Sequence 29, Appl
30	123	1.4	19608	4	US-10-084-846A-8	Sequence 8, Appl1
31	122.5	1.4	2063	3	US-09-918-715-204	Sequence 204, App
32	122.5	1.4	2063	4	US-10-474-794-204	Sequence 204, App
33	122.5	1.4	2063	5	US-10-979-159-204	Sequence 204, App
34	122	1.4	2379	5	US-10-211-028-7	Sequence 7, Appl1
35	122	1.4	2639	5	US-10-450-763-45375	Sequence 45375, A
36	121	1.4	764	4	US-10-369-493-18081	Sequence 18081, A
37	121	1.4	764	4	US-10-389-566-1010	Sequence 1010, Ap
38	119.5	1.4	4572	5	US-10-042-665A-4	Sequence 4, Appl1
39	119.5	1.4	4599	3	US-09-976-059-15	Sequence 15, Appl
40	119	1.4	826	5	US-10-732-923-6777	Sequence 6777, Ap
41	119	1.4	1387	4	US-10-156-761-13000	Sequence 13000, A
42	118.5	1.4	799	4	US-10-369-493-10623	Sequence 10623, A
43	118	1.4	926	4	US-10-282-122A-62076	Sequence 62076, A
44	118	1.4	1217	4	US-10-369-493-11861	Sequence 11861, A
45	118	1.4	2220	4	US-10-389-566-802	Sequence 802, App

ALIGNMENTS

```

RESULT 1
US-10-757-832-2
/ Sequence 2, Application US/10757832
/ Publication No. US20050037016A1
/
GENERAL INFORMATION:
/ APPLICANT: VIRGIN, HERBERT W.
/ TITLE OF INVENTION: MORINE CALICIVIRUS
/ FILE REFERENCE: 56029-45752
/ CURRENT APPLICATION NUMBER: US/10/757, 832
/ PRIOR FILING DATE: 2004-01-14
/ PRIOR APPLICATION NUMBER: 60/440, 016
/ NUMBER OF SEQ ID NOS: 54
/ SOFTWARE: PatentIn version 3.2
/ SEQ ID NO 2
/ LENGTH: 1625
/ TYPE: PRT
/ ORGANISM: Murine Norovirus type 1
/
FEATURES:
/ NAME/KEY: misc feature
/ LOCATION: (145)..(145)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (282)..(282)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (299)..(299)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (316)..(316)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (327)..(327)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (453)..(453)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (544)..(544)
/ OTHER INFORMATION: Variable amino acid
/
FEATURE:
/ NAME/KEY: misc feature
/ LOCATION: (559)..(559)
/ OTHER INFORMATION: Variable amino acid

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:39:38 ; Search time 238.89 Seconds
(without alignments)
2988.783 Million cell updates/sec

Title: US-10-757-832-2

Perfect score: 8514
Sequence: 1 MTPPEQEAQPGALALAHAG.....MVVPPPPICFALGALMNNGC 1625

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_21.*
1: geneseqp19808.*
2: geneseqp19908.*
3: geneseqp20008.*
4: geneseqp20018.*
5: geneseqp20028.*
6: geneseqp20038.*
7: geneseqp20048.*
8: geneseqp20058.*
9: geneseqp20068.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	ID	Description
1	8474	99.5	1625	ADY21359
2	3572	42.0	1738	AAR50971
3	3572	42.0	1738	ADP72175
4	3572	42.0	1738	ADP96371
5	1522.5	17.9	510	ADZ79314
6	784	9.2	286	AAR57092
7	394	4.6	127	AAR12298
8	394	4.6	127	ADP72180
9	381	4.5	2292	ADZ15037
10	379.5	4.5	126	AAR50977
11	375	4.4	2292	ADZ15034
12	372	4.4	2292	ADZ15035
13	371.5	4.4	2303	ADZ15041
14	370.5	4.4	2292	ADZ15033
15	370	4.3	2293	ADZ15038
16	368	4.3	2292	ADZ15036
17	365.5	4.3	2303	ADZ15039
18	362	4.2	2179	ADJ92013
19	361.5	4.0	1890	ADZ15011
20	343.5	4.0	2307	ADZ15042
21	337.5	3.8	2164	AAP81045
22	337	3.8	2164	AAP80131
23	320			
24	320			

Description

ADY21359 Murine no
AAR50971 Norwalk v
ADP72175 Norwalk v
ADP96371 Norwalk v
ADZ79314 Norwalk v
AAR57092 Small rou
AAR12298 Norwalk v
ADP72180 Norwalk v
ADZ15037 EMCV-PV2
AAR50977 Norwalk v
ADZ15034 EMCV-B pr
ADZ15035 EMCV-Da p
ADZ15041 TMEV/Beau
ADZ15033 EMCV-meng
ADZ15036 EMCV-meng
ADZ15039 EMCV-R pr
ADJ92013 TMEV/GDI
ADZ15011 Human par
ADZ15042 TIV-NGS91
AAP81045 Sequence
AAP80131 Peptides

25	319	3.7	2227	1	AAP60066	AAP60066 Sequence
26	319	3.7	2227	5	AAR19899	AAR19899 Hepatitis
27	319	3.7	2227	7	ABW00350	ABW00350 Hepatitis
28	316.5	3.7	2332	8	ADV94875	ADV94875 O-type fo
29	315	3.7	2306	2	AAR22210	AAR22210 True type
30	314	3.7	2247	2	AAR27126	AAR27126 Equine rh
31	309	3.6	2227	2	AAR34074	AAR34074 Hepatitis
32	309	3.6	2227	3	ABG11727	ABG11727 Amino aci
33	309	3.6	2227	5	ABG11727	ABG11727 Wild-type
34	309	3.6	2227	6	ABU08639	ABU08639 Wild-type
35	306	3.6	2150	1	AAP60045	AAP60045 Sequence
36	306	3.6	2150	2	AAP81048	AAP81048 Sequence
37	306	3.6	2150	2	AAR05127	AAR05127 Complete
38	306	3.6	2227	2	AAR05697	AAR05697 Attenuate
39	305	3.6	2209	1	AAP20037	AAP20037 Sequence
40	304	3.6	2227	3	ABG11728	ABG11728 Amino aci
41	304	3.6	2227	5	ABU08640	ABU08640 Hepatitis
42	304	3.6	2227	6	ADW22753	ADW22753 Foot-and-
43	304	3.6	2232	7	ADW22753	ADW22753 Foot-and-
44	303.5	3.6	2232	9	ABG11728	ABG11728 Amino aci
45	302	3.5	2227	3	ABG11728	ABG11728 Amino aci

ALIGNMENTS

RESULT 1	ADY21359	standard; protein; 1625 AA.
ID	ADY21359	
XX	ADY21359;	
AC	ADY21359;	
DT	05-MAY-2005	(first entry)
DE	Murine norovirus 1 (MNV-1) consensus DNA ORF1 protein.	
XX		
XX		
KW	Diagnosis; enteritis; antiinflammatory; gastrointestinal gen.;	
KW	gastroenteritis; gastrointestinal disease; inflammation; virulence;	
KW	vaccine; animal disease model.	
XX		
OS	Murine norovirus 1.	
XX		
XX		
FT	Key	Location/Qualifiers
FT	Misc-difference 145	/note= "Xaa equals variable amino acid"
FT	Misc-difference 280	/note= "Encoded by GTR"
FT	Misc-difference 282	/note= "Xaa equals variable amino acid"
FT	Misc-difference 299	/note= "Xaa equals variable amino acid"
FT	Misc-difference 318	/note= "Xaa equals variable amino acid"
FT	Misc-difference 327	/note= "Xaa equals variable amino acid"
FT	Misc-difference 379	/note= "Xaa equals variable amino acid"
FT	Misc-difference 397	/note= "Encoded by CTD"
FT	Misc-difference 453	/note= "Encoded by CTV"
FT	Misc-difference 544	/note= "Xaa equals variable amino acid"
FT	Misc-difference 544	/note= "Xaa equals variable amino acid"
FT	Misc-difference 559	/note= "Xaa equals variable amino acid"
FT	Misc-difference 579	/note= "Xaa equals variable amino acid"
FT	Misc-difference 601	/note= "Xaa equals variable amino acid"
FT	Misc-difference 661	/note= "Encoded by TCY"
FT	Misc-difference 668	/note= "Xaa equals variable amino acid"
FT	Misc-difference 671	/note= "Xaa equals variable amino acid"
FT	Misc-difference 671	/note= "Xaa equals variable amino acid"

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Comugen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 13:42:44 / Search time 49.2839 Seconds
(without alignments)
3172.480 Million cell updates/sec

Title: US-10-757-832-2

Perfect score: 8514
Sequence: 1 MTPPEQEAQPGALALHAEG.....MVPPTPICPALGALWNNGC 1625

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3560	41.8	1737	2 A37491	hypothetical helic
2	995	11.7	306	2 E37471	hypothetical helic
3	973	11.4	333	2 S60615	RNA-directed RNA p
4	850.5	10.0	352	2 C37471	hypothetical helic
5	769.5	9.0	1763	1 RRMWP9	genome polypeptid
6	760.5	8.9	1762	2 T09245	genome polypeptid
7	731.5	8.6	2344	2 S55399	genome polypeptid
8	717.5	8.4	2344	2 S55399	genome polypeptid
9	711	8.4	1287	2 A43488	genome polypeptid
10	709.5	8.3	2344	1 RRMWP9	genome polypeptid
11	523.5	6.1	211	2 D37471	hypothetical helic
12	381	4.5	2292	1 S55401	hypothetical helic
13	375	4.4	2292	1 GNNYB	genome polypeptid
14	372	4.4	2292	1 GNNYB	genome polypeptid
15	371.5	4.4	2303	1 GNNYB	genome polypeptid
16	370.5	4.4	2292	2 S35961	capsid polypeptid
17	361.5	4.2	2301	1 GNNYB	genome polypeptid
18	361	4.2	2303	1 GNNYB	genome polypeptid
19	361	4.2	2303	1 GNNYB	genome polypeptid
20	359.5	4.2	2290	1 GNNYB	genome polypeptid
21	347.5	4.1	2175	1 GNNYB	genome polypeptid
22	326	3.8	2214	1 A48548	genome polypeptid
23	324	3.8	2205	1 GNNYB	genome polypeptid
24	324	3.8	2205	1 GNNYB	genome polypeptid
25	320	3.8	2164	1 GNNYB	genome polypeptid
26	319	3.7	2207	1 S09553	genome polypeptid
27	319	3.7	2227	1 GNNYB	genome polypeptid
28	318.5	3.7	381	2 A40481	RNA-directed RNA p
29	313	3.7	2194	1 GNNYB	genome polypeptid

30	312	3.7	2333	1 GNNYB	genome polypeptid
31	310	3.6	2206	1 GNNYB	genome polypeptid
32	310	3.6	2207	1 GNNYB	genome polypeptid
33	309.5	3.6	2230	1 GNNYB	genome polypeptid
34	309	3.6	2237	1 GNNYB	genome polypeptid
35	308.5	3.6	2232	1 GNNYB	genome polypeptid
36	307	3.6	2312	1 GNNYB	genome polypeptid
37	306.5	3.6	2206	2 S03822	genome polypeptid
38	305.5	3.6	2157	1 GNNYB	genome polypeptid
39	305	3.6	2209	1 GNNYB	genome polypeptid
40	305	3.6	2236	2 S37077	genome polypeptid
41	305	3.6	2227	1 GNNYB	genome polypeptid
42	304	3.6	2207	1 GNNYB	genome polypeptid
43	303.5	3.6	2227	1 GNNYB	genome polypeptid
44	303.5	3.6	2227	1 GNNYB	genome polypeptid
45	302	3.5	2179	1 GNNYB	genome polypeptid

ALIGNMENTS

RESULT 1

A37491 hypothetical helicase/polymersase polypeptid - Southampton virus

N/Alternate names: orf1 protein

C/Species: Southampton virus

C/Date: 03-Mar-1994 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004

C/Accession: A37491

R/Lambden, P.R.; Caul, B.O.; Ashley, C.R.; Clarke, I.N.

Science 259, 516-519, 1993

A/Title: Sequence and genome organization of a human small round-structured (Norwalk-like

A/Reference number: A37491, MID:93142023, PMID:8380940

A/Contents: small round-structured virus, SRSV, Norwalk virus, Norwalk-like virus, SRSV

A/Accession: A37491

A/Status: preliminary; not compared with conceptual translation

A/Molecule type: genomic RNA

A/Residues: 1-1737 <LAMB>

A/Cross-references: UNIPROT:004544; UNIPARC:UP100001757D7

A/Note: sequence extracted from NCBI backbone (NCBI:123456)

C/Superfamily: rabbit calicivirus RNA-polymersase

Query Match	41.8%; Score 3560; DB 2; Length 1737;
Best Local Similarity	44.0%; Pred. No. 8.6e-245;
Matches 713; Conservative 270; Mismatches 512; Indels 126; Gaps 20;	
QY 73 PDAPSHADAMADAKPEYIGTILSDDKKFTHYSYIIGGLVMGYNNPDAVCOATIDVEK 132	
DB 126 PLPPIDLRNRPASBPITGMIFFRGHIVHSIYIIGQGTGVSPOAASVAVRTIOP 185	
QY 133 LHLMPWPV--EPRXPLDSALRKCVGMTVPVATVNCVOCWIVIGIDTWLKRKIS 190	
DB 186 IAAWNRVCYIPQKHRSYDQKLENEBPVVAITNCFPCQVNNLSDITMLQRLVT 245	
QY 191 RDPFYSVQDWMVNDQEPFIPSKLNVSDGILVALSAVGRPIKXNLASVKEPIINIV 250	
DB 246 SG-RFHHPQSWGQCPPEPQDSKELIVRDALLAANGLVSGPPKNTLGLKPLNVNITL 304	
QY 251 LSCDWTFSGLVNALILLALFDFIPTPTDYTKMISIFGWOAGRPDXALDVPTLLGG 310	
DB 305 SDCDWTFSGLVNALILLALFDFIPTPTDYTKMISIFGWOAGRPDXALDVPTLLGG 364	
QY 311 IGNAFGXSEITRKXSTNSALKAQBMGKFAIVKQIMAMTWSEDPVPLLSMBO 370	
DB 365 IGLAIGTRDKTKVWMSAVDGLAANTQDQYGLFSLIKCTFF-GGDQERTLKIGEA 423	
QY 371 AIIKNECOLENTLMLRDNAGAPLRSIDBEOBVRKLIACGNSATYGTNALLARI 430	
DB 424 AVIDMVLSTSTYGLVRDQAKAKAMNILDNEBKRKLSANADPHVISTTALLSRI 483	
QY 431 SNAAPAFKRAAQTSVRPVVVMVSGRPGIGTCPCQNLAKIPLASLDETSYGLIPRA 490	
DB 484 SNAASLAKAQAEMLTSMRPVVMVVMVSGRPGIGTCPCQNLAKIPLASLDETSYGLIPRA 543	

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 14:12:48 / Search time 60.2359 seconds

(without alignments)
2230.364 Million cell updates/sec

Title: US-10-757-832-2

Sequence: 1 MTPPQHAQPGALAHMG.....MVPFPICFALGALMNGC 1625

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 10%
Listing first 45 summaries

Database:

- 1: /cgn2_6/ptodata/1/1aa/5_COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/6_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/7_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/8_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/9_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/10_COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	3572	42.0	1738	2 US-08-486-049-2	Sequence 2, Appl1
2	3572	42.0	1738	2 US-10-314-739A-2	Sequence 2, Appl1
3	379.5	4.5	126	2 US-10-314-739A-7	Sequence 7, Appl1
4	319	3.7	2227	2 US-10-104-966-12	Sequence 12, Appl1
5	319	3.7	2227	2 US-09-929-955-12	Sequence 12, Appl1
6	315	3.7	2232	2 US-09-091-219-25	Sequence 25, Appl1
7	315	3.7	2232	2 US-09-660-541-25	Sequence 25, Appl1
8	315	3.7	2247	2 US-09-091-219-2	Sequence 2, Appl1
9	315	3.7	2247	2 US-09-660-541-2	Sequence 2, Appl1
10	310	3.6	2206	1 US-07-852-260-2	Sequence 2, Appl1
11	310	3.6	2206	1 US-08-461-503-2	Sequence 2, Appl1
12	310	3.6	2206	1 US-08-465-250-2	Sequence 2, Appl1
13	309	3.6	2227	2 US-08-475-886-2	Sequence 2, Appl1
14	309	3.6	2227	2 US-08-397-332-2	Sequence 2, Appl1
15	309	3.6	2227	2 US-09-171-387-2	Sequence 2, Appl1
16	309	3.6	2227	2 US-09-653-499-2	Sequence 2, Appl1
17	309	3.6	2227	2 US-10-135-988-2	Sequence 2, Appl1
18	306	3.6	2318	2 US-09-091-219-24	Sequence 24, Appl1
19	306	3.6	2318	2 US-09-660-541-24	Sequence 24, Appl1
20	304	3.6	2227	2 US-08-475-886-4	Sequence 4, Appl1
21	304	3.6	2227	2 US-09-653-499-4	Sequence 4, Appl1
22	304	3.6	2227	2 US-10-135-988-4	Sequence 4, Appl1
23	302	3.5	2227	2 US-08-475-886-6	Sequence 6, Appl1
24	302	3.5	2227	2 US-08-397-332-4	Sequence 4, Appl1
25	302	3.5	2227	2 US-09-653-499-6	Sequence 6, Appl1
26	302	3.5	2227	2 US-10-135-988-6	Sequence 6, Appl1
27	204	2.4	3457	1 US-08-416-603-4	Sequence 4, Appl1

28	194.5	2.3	3443	1 US-08-416-603-2	Sequence 2, Appl1
29	177	2.1	652	2 US-10-272-459-48	Sequence 48, Appl1
30	174	2.0	1416	1 US-08-061-465-4	Sequence 4, Appl1
31	173.5	2.0	516	2 US-09-496-320-13	Sequence 13, Appl1
32	163	1.9	495	6 5516630-4	Patent No. 5516630
33	152.5	1.8	627	2 US-10-222-100-3	Sequence 3, Appl1
34	148.5	1.7	512	2 US-09-496-320-12	Sequence 12, Appl1
35	142.5	1.7	3816	2 US-09-428-517-3	Sequence 3, Appl1
36	126	1.5	126	2 US-09-902-540-15442	Sequence 15442, A
37	125.5	1.5	126	2 US-10-314-739A-14	Sequence 14, Appl1
38	125	1.5	527	2 US-09-900-920-61	Sequence 61, Appl1
39	119.5	1.4	4572	2 US-10-042-665A-4	Sequence 4, Appl1
40	118	1.4	314	2 US-09-583-545-15	Sequence 15, Appl1
41	117	1.4	314	2 US-09-514-245-24	Sequence 24, Appl1
42	117	1.4	566	2 US-09-514-245-18	Sequence 18, Appl1
43	117	1.4	703	2 US-09-902-540-11194	Sequence 11194, A
44	117	1.4	4630	2 US-09-091-609-2	Sequence 2, Appl1
45	117	1.4	5215	2 US-09-103-537-2	Sequence 2, Appl1

ALIGNMENTS

```

RESULT 1
US-08-486-049-2
/ Sequence 2, Application US/08486049
/ Patent No. 6572862
/ GENERAL INFORMATION:
/ APPLICANT: Bates, Mary K
/ APPLICANT: Jiang, Xi
/ APPLICANT: Graham, David Y
/ TITLE OF INVENTION: Methods and Reagents to Detect and
/ NUMBER OF INVENTION: Characterize No. 6572862walk and Related Viruses
/ CORRESPONDENCE ADDRESS:
/ ADDRESSER: Fulbright & Jaworski L.L.P.
/ STREET: 801 Pennsylvania Ave., N.W.
/ CITY: Washington, D.C.
/ STATE:
/ COUNTRY: USA
/ ZIP: 20004
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ COMPUTER: IBM PC compatible
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.25
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/08/486,049
/ FILING DATE: June 7, 1995
/ CLASSIFICATION: 435
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Davis, Peter
/ REGISTRATION NUMBER: 36,119
/ REFERENCE/DOCKET NUMBER: 311,023
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 202-662-0200
/ TELEFAX: 202-662-4643
/ TELEX:
/ INFORMATION FOR SEQ ID NO: 2:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1738 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-08-486-049-2

Query Match      42.0% Score 3572; DB 2; Length 1738;
Best Local Similarity 44.2%; Pred. No. 0;
Matches 720; Conservative 257; Mismatches 517; Indels 136; Gaps 20;

Cy 66 LRPKRDPAASHADANAKRPVIGSLBDHKKFYHVSIVYIGGLWGVNPNPSAAYQC 125
Db 126 LRPVDRSTP-----ATEPTIGDWIEFTYEGHIVYALTYIGGKIVGVHSPDAPRSI 177

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:42:44 ; Search time 16.4078 Seconds
(without alignments) 3172.480 Million cell updates/sec

Title: US-10-757-832-3

Perfect score: 2838

Sequence: 1 MRMSDGAAPKANGSEBASGD.....PRVQLASVLSLNGRMKQ 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 80:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	992.5	35.0	542	2 S60616	capsid protein - h
2	980	34.5	539	2 S40111	capsid protein - h
3	970.5	34.2	546	2 B37491	major capsid prote
4	958.5	33.8	530	2 B37471	capsid protein - N
5	310.5	10.9	576	2 A53982	capsid protein - E
6	308.5	10.9	702	2 A48562	coat protein - San
7	306.5	10.8	2344	2 S55399	genome polypotein
8	301.5	10.6	2344	2 S64740	genome polypotein
9	300.5	10.6	2344	1 RRMWRH	genome polypotein
10	278	9.8	703	1 C48562	coat protein - San
11	264.5	9.3	668	1 VCMWPC	coat protein - fel
12	250	8.8	668	2 UQ2354	capsid protein - f
13	249	8.7	671	1 VCMWF9	coat protein - fel
14	246	8.7	668	2 UQ2356	capsid protein - f
15	241	8.5	668	1 VCMWPF	coat protein - fel
16	135	4.8	757	2 JS0198	genome polypotein
17	120	4.2	733	2 JQ1892	capsid protein - f
18	120	4.2	2336	2 S37077	genome polypotein
19	117.5	4.1	2332	1 GNNYF	genome polypotein
20	116.5	4.1	733	2 JQ1891	capsid protein - f
21	116.5	4.1	2333	1 GNNY2P	genome polypotein
22	115.5	4.1	511	2 C70803	hypothetical prote
23	112	3.9	3473	1 A46112	genome polypotein
24	112	3.9	3473	2 S27927	polypotein - rice
25	111	3.9	1324	2 S06187	RNA2 polypotein -
26	110.5	3.9	1011	1 GNNY1	genome polypotein
27	109.5	3.9	1693	1 MAMWHE	genome polypotein
28	109	3.8	329	2 C97560	hypothetical prote
29	109	3.8	329	2 AB2781	amidohydrolase (im

30	108.5	3.8	2292	2 S35961	capsid polypotein
31	108	3.8	2194	1 GNNYB7	genome polypotein
32	105	3.7	2332	2 GNNY4F	genome polypotein
33	105	3.7	3573	2 S23070	erythronolide synt
34	104.5	3.7	1706	2 B75633	probable RNA helic
35	104	3.7	575	2 T11753	mullerian inhibiti
36	103.5	3.6	476	2 T42692	hypothetical prote
37	103.5	3.6	1686	2 A87692	conserved hypotet
38	103.5	3.6	2206	2 S03822	genome polypotein
39	103.5	3.6	2292	1 GNNYB	genome polypotein
40	103.5	3.6	2292	2 S55401	capsid polypotein
41	103	3.6	1809	2 S57329	tuberosus sclerosi
42	101.5	3.6	2206	1 GNNY4P	genome polypotein
43	101.5	3.6	2206	1 GNNY27	genome polypotein
44	100.5	3.5	647	2 T35931	probable gamma-glu
45	100	3.5	307	2 B83129	homoprotocatechua

ALIGNMENTS

RESULT 1

S60616 capsid protein - human calicivirus (strain Melksham)

C:Species: human calicivirus

A:Variety: strain Melksham

C:Date: 23-May-1997 #sequence_revision 23-May-1997 #text_change 09-Jul-2004

C:Accession: S60616

R:Green, S.M.; Lambden, P.R.; Gaul, E.O.; Ashley, C.R.; Clarke, I.N.

A:Title: Capsid diversity in small round-structured viruses: molecular characterization

A:Reference number: S60615; PMID:9613658; PMID:8533462

A:Accession: S60616

A:Molecule type: genomic RNA

A:Residues: 1-542 <GR>

A:Cross-references: UNIPROT:066293; UNIPARC:U0100000ED1PA; EMBL:X81879; NID:9976077; PI

A:Experimental source: strain Melksham

A:Note: It is uncertain whether Met-1 or Met-3 is the initiator

C:Superfamily: human calicivirus capsid protein

C:Keywords: capsid protein; coat protein

Query Match 35.0%; Score 992.5; DB 2; Length 542;
Best Local Similarity 42.0%; Pred. No. 2.3e-71;
Matches 233; Conservative 79; Mismatches 208; Indels 35; Gaps 14;

QY	1	MEM-SDGAAPKANGSEBASGDIVPAAYVXQVPAAGALAPAAAGTNOIXPMTFQNP	59
DB	1	MEM-SDGAAPKANGSEBASGDIVPAAYVXQVPAAGALAPAAAGTNOIXPMTFQNP	56
QY	60	VOCPIGBPISPRNTGPIPLDLPALGPNPILAHLSAMVTGVMGXKRYQLVLGNAFTA	119
DB	57	VQAPNGEFTVSRNAPGKVLNLELPILAHLSAMVTGVMGXKRYQLVLGNAFTA	116
QY	120	GRVVALVPPYPPKSLTAAQITCEPHWCDVKTLEPIQLPLDVRVLMHATQDBESM	179
DB	117	GLVPAAYVPPHPEVNTLSPKLTMTPEHVIDRTLEPVLLPLPDVANSFHHYQKDPKM	176
QY	180	RIVCMULTYPLKRNPSQDESFVSGRLSKPADPNNVLTLPPIERTYMWVDPVQPLR	239
DB	177	RIVAMULTYPLKRNPSQDESFVSGRLSKPADPNNVLTLPPIERTYMWVDPVQPLR	236
QY	240	CTHARWPAVYGLVDPSPNPNQNGRVHVDGTLTGTTPLSGSVWSCFAXAAVKKFOS	299
DB	237	LSNSRFPVVIDMTYSFNVISVQCNQNGCTIDGELGTTQGVSGICAFKGVTAHMD	296
QY	300	GTGVAATFTLLBODGSAVYG-DRAAPGLPRFLMATGDRGPDRIHQWRQAGH----	353
DB	297	NDHLANNVITITNNGSPFPDSBDIPALGVPPFGQGVFVGSORDKON---AAGSHBPAN	352
QY	354	--HFMILGPTTNADAPYQGVAFASVTAAASLDLVGRVAVRNSIYGRQDI-----	404
DB	353	RGHDAVV--FTYTAQYTPKGOIQIGTQOTDDL-TVNGPVKCTP---VGLNTEHFNQWV	406

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 14:13:00 / Search time 65.631 Seconds

(without alignments)
3444.190 Million cell updates/sec

Title: US-10-757-832-3

Perfect score: 2838
Sequence: 1 MRMSDGAAPRANGSEASGCD.....PRUYQLASVGLATGRMLKQ 541

Scoring table: BLOSUM62

Gapop 10.0, Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database:

Published Applications AA Main:
1: /cgm2_6/ptcdat1/pubpaa/US07_PUBCOMB.pep:*
2: /cgm2_6/ptcdat1/pubpaa/US08_PUBCOMB.pep:*
3: /cgm2_6/ptcdat1/pubpaa/US09_PUBCOMB.pep:*
4: /cgm2_6/ptcdat1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgm2_6/ptcdat1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgm2_6/ptcdat1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2830	99.7	541	US-10-757-832-3	Sequence 3, Appl1
2	982.5	34.6	542	US-10-950-163-30	Sequence 30, Appl1
3	958.5	33.8	530	US-10-314-739-3	Sequence 3, Appl1
4	958.5	33.8	530	US-10-895-791-2	Sequence 2, Appl1
5	958.5	33.8	530	US-10-895-791-6	Sequence 6, Appl1
6	958.5	33.8	530	US-10-895-791-7	Sequence 7, Appl1
7	953.5	33.6	530	US-10-950-163-28	Sequence 28, Appl1
8	953.5	33.6	530	US-10-950-163-29	Sequence 29, Appl1
9	260.5	9.2	669	US-10-209-507-2	Sequence 2, Appl1
10	252	8.9	668	US-10-209-507-4	Sequence 4, Appl1
11	249	8.8	547	US-10-670-695-4	Sequence 4, Appl1
12	249	8.8	671	US-10-670-695-2	Sequence 2, Appl1
13	249	8.8	671	US-10-769-531-1	Sequence 1, Appl1
14	248	8.7	668	US-10-769-531-2	Sequence 2, Appl1
15	247.5	8.7	667	US-10-769-531-3	Sequence 3, Appl1
16	142.5	5.0	618	US-10-769-531-4	Sequence 4, Appl1
17	118.5	4.2	736	US-10-863-637-7	Sequence 7, Appl1
18	117	4.1	3970	US-10-156-761-10429	Sequence 10429, A
19	116.5	4.1	1147	US-10-327-481A-38	Sequence 38, Appl1
20	115.5	4.1	511	US-10-080-170-641	Sequence 641, Appl1
21	115.5	4.1	511	US-10-080-170-641	Sequence 641, Appl1
22	115.5	4.1	511	US-10-468-356-641	Sequence 641, Appl1
23	115.5	4.1	511	US-10-510-021-67	Sequence 67, Appl1
24	111	3.9	1203	US-10-369-493-8333	Sequence 8333, Appl1
25	109.5	3.8	1693	US-09-851-410-7	Sequence 7, Appl1
26	108	3.8	5245	US-10-329-079-45	Sequence 45, Appl1
27	107	3.8	1073	US-10-925-357-7	Sequence 7, Appl1

28	104.5	3.7	2914	US-10-093-463-82	Sequence 82, Appl1
29	103	3.6	1700	US-09-734-402-2	Sequence 2, Appl1
30	102	3.6	1121	US-09-734-402-1	Sequence 1, Appl1
31	101.5	3.6	1073	US-10-156-761-8117	Sequence 8117, Appl1
32	101	3.5	995	US-10-450-763-52543	Sequence 52543, Appl1
33	100.5	3.5	1198	US-10-156-761-8467	Sequence 8467, Appl1
34	100	3.5	307	US-09-815-242-5155	Sequence 5155, Appl1
35	100	3.5	307	US-10-282-122A-43599	Sequence 43599, Appl1
36	100	3.5	701	US-10-156-761-9875	Sequence 9875, Appl1
37	99.5	3.5	894	US-09-223-490-34	Sequence 34, Appl1
38	99.5	3.5	894	US-09-236-939-34	Sequence 34, Appl1
39	99.5	3.5	894	US-10-646-760-34	Sequence 34, Appl1
40	99.5	3.5	894	US-10-696-909A-4	Sequence 4, Appl1
41	99.5	3.5	894	US-10-631-467-609	Sequence 609, Appl1
42	99.5	3.5	1062	US-10-389-566-608	Sequence 608, Appl1
43	99.5	3.5	1668	US-10-732-923-8865	Sequence 8865, Appl1
44	99.5	3.5	1828	US-10-221-625-15	Sequence 15, Appl1
45	99.5	3.5	2971	US-10-146-473-50	Sequence 50, Appl1

ALIGNMENTS

```

RESULT 1
US-10-757-832-3
Sequence 3, Application US/10757832
Publication No. US20050037016A1
GENERAL INFORMATION:
APPLICANT: VIRGIN, HERBERT W.
TITLE OF INVENTION: MURINE CALICIVIRUS
FILE REFERENCE: 56029-45752
CURRENT APPLICATION NUMBER: US/10/757, 832
CURRENT FILING DATE: 2004-01-14
PRIOR APPLICATION NUMBER: 60/440,016
PRIOR FILING DATE: 2003-01-14
NUMBER OF SEQ ID NOS: 54
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
LENGTH: 541
TYPE: PRT
ORGANISM: Murine Norovirus type 1
FEATURE:
NAME/KEY: misc feature
LOCATION: (32)..(32)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (52)..(52)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (106)..(106)
OTHER INFORMATION: Variable amino acid
FEATURE:
NAME/KEY: misc feature
LOCATION: (291)..(291)
OTHER INFORMATION: Variable amino acid
US-10-757-832-3
Query Match 99.7% Score 2830, DB 5, Length 541,
Best Local Similarity 100.0%, Pred. No. 2.1e-256,
Matches 541, Conservative 0, Mismatches 0, Indels 0, Gaps 0;
QY 1 MRMSDGAAPRANGSEASGCDLVPAAVEAQPVAAGALAAADAGQINIXPWFQNFV 60
Db 1 MRMSDGAAPRANGSEASGCDLVPAAVEAQPVAAGALAAADAGQINIXPWFQNFV 60
QY 61 QCPYGRSISPRTPGRIIFDLALGRLNPLYLAHLSMTTGGWGNKXEVQVLGNATFAG 120
Db 61 QCPYGRSISPRTPGRIIFDLALGRLNPLYLAHLSMTTGGWGNKXEVQVLGNATFAG 120
QY 121 KVVVALVPPPPPGSLTTAQTCTCPHYMCDVRLTLPQLFLDLVRRYLMMATDQBSMR 180
Db 121 KVVVALVPPPPPGSLTTAQTCTCPHYMCDVRLTLPQLFLDLVRRYLMMATDQBSMR 180

```


GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 14:12:48 / Search time 20.0539 Seconds
(without alignments)
2230.364 Million cell updates/sec

Title: US-10-757-832-3

Sequence: 1 MEMSDGAAPKANGSEASGQD.....PLUYOLASVGSATGMLKQ 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/prodata/1/1aa/5 COMB.pep.*
2: /cgn2_6/prodata/1/1aa/6 COMB.pep.*
3: /cgn2_6/prodata/1/1aa/7 COMB.pep.*
4: /cgn2_6/prodata/1/1aa/8 COMB.pep.*
5: /cgn2_6/prodata/1/1aa/9 COMB.pep.*
6: /cgn2_6/prodata/1/1aa/10 COMB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	958.5	33.8	530	US-08-486-049-3	Sequence 3, App1
2	958.5	33.8	530	US-10-314-739A-3	Sequence 3, App1
3	260.5	9.2	669	US-09-617-594A-2	Sequence 2, App1
4	260.5	9.2	669	US-10-209-507-2	Sequence 2, App1
5	253	8.9	626	US-09-590-020-7	Sequence 4, App1
6	252	8.9	668	US-10-209-507-4	Sequence 4, App1
7	244	8.6	623	US-09-590-020-2	Sequence 4, App1
8	244	8.6	623	US-09-590-020-4	Sequence 4, App1
9	244	8.6	623	US-09-590-020-6	Sequence 4, App1
10	233	8.2	622	US-09-590-020-6	Sequence 4, App1
11	117.5	4.1	2318	US-09-091-219-24	Sequence 24, App1
12	117.5	4.1	2318	US-09-660-541-24	Sequence 24, App1
13	109.5	3.9	1042	US-09-252-991A-30444	Sequence 30444, A
14	109.5	3.9	1693	US-08-478-507-7	Sequence 7, App1
15	109.5	3.9	1693	US-09-128-275A-7	Sequence 7, App1
16	109.5	3.9	1693	US-09-553-427-7	Sequence 7, App1
17	108.5	3.8	3567	US-07-642-734C-4	Sequence 4, App1
18	108.5	3.8	3567	US-08-439-009A-4	Sequence 4, App1
19	103.5	3.6	2206	US-07-852-260-2	Sequence 2, App1
20	103.5	3.6	2206	US-08-461-503-2	Sequence 2, App1
21	103.5	3.6	2206	US-08-465-250-2	Sequence 2, App1
22	102	3.6	3457	US-08-416-603-4	Sequence 4, App1
23	100	3.5	755	US-09-252-991A-28386	Sequence 28386, A
24	99.5	3.5	894	US-08-372-892-2	Sequence 2, App1
25	99.5	3.5	894	US-08-445-640-34	Sequence 34, App1
26	99.5	3.5	894	US-08-170-558-34	Sequence 34, App1
27	99.5	3.5	894	US-08-447-314-34	Sequence 34, App1

28	99.5	3.5	894	US-08-445-461-34	Sequence 34, App1
29	99.5	3.5	894	US-09-223-490-34	Sequence 34, App1
30	99.5	3.5	975	US-09-949-016-7595	Sequence 7595, App1
31	99.5	3.5	2972	US-09-579-181-2	Sequence 2, App1
32	99.5	3.5	3118	US-09-579-181-1	Sequence 1, App1
33	97.5	3.4	888	US-08-445-640-35	Sequence 35, App1
34	97.5	3.4	888	US-08-170-558-35	Sequence 35, App1
35	97.5	3.4	888	US-08-447-314-35	Sequence 35, App1
36	97.5	3.4	888	US-08-445-461-35	Sequence 35, App1
37	97.5	3.4	888	US-09-223-490-35	Sequence 35, App1
38	96	3.4	723	US-09-893-737-100	Sequence 100, App1
39	95.5	3.4	623	US-08-653-740-7	Sequence 7, App1
40	95.5	3.4	623	US-09-073-594-7	Sequence 7, App1
41	95.5	3.4	623	US-09-275-925-7	Sequence 7, App1
42	95.5	3.4	3729	US-08-804-227C-4	Sequence 4, App1
43	95	3.3	669	US-09-949-016-6887	Sequence 6887, App1
44	95	3.3	677	US-09-949-016-8351	Sequence 8351, App1
45	94.5	3.3	1206	US-09-252-991A-19632	Sequence 19632, A

ALIGNMENTS

RESULT 1
US-08-486-049-3
Sequence 3, Application US/08486049
Patent No. 6572862
GENERAL INFORMATION:
APPLICANT: Bates, Mary K
APPLICANT: Jiang, Xi
APPLICANT: Graham, David Y
TITLE OF INVENTION: Methods and Reagents to Detect and
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESSER: Fulbright & Jaworski L.L.P.
STREET: 801 Pennsylvania Ave., N.W.
CITY: Washington, D.C.
STATE:
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,049
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Davis, Peter
REGISTRATION NUMBER: 36,119
REFERENCE/DOCKET NUMBER: 311.023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-662-0200
TELEFAX: 202-662-4643
TELEX:
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-049-3
Query Match 33.8%, Score 958.5, DB 2, Length 530;
Best Local Similarity 40.6%, Pred. No. 2.6e-91;
Matches 223, Conservative 79, Mismatches 208, Indels 39, Gaps 11;
QY 1 MEMSDGAAPKANGSEASGQDVFPA-VEQAVXQPVAGALAPAPAGQINQIXPMIFQNF 59
DB 2 MEMSDAASSVDGASGAGQ-LVPEVNASDPLAMDVVASSTVAIVAGQVNPIDPITINN 60

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:39:38 / Search time 79.532 Seconds
(without alignments)
2988.783 Million cell updates/sec

Title: US-10-757-832-3

Perfect score: 2838
Sequence: 1 NMSDGAAPKANGSRAAGD.....PRLYOLASVGLATGRMLKQ 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

A_Geneseq_21:.*
1: geneseq1980s:.*
2: geneseq1990s:.*
3: geneseq2000s:.*
4: geneseq2001s:.*
5: geneseq2002s:.*
6: geneseq2003as:.*
7: geneseq2003bs:.*
8: geneseq2004s:.*
9: geneseq2005s:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARYS

Result No.	Score	Query Match	Length	ID	Description
1	2830	99.7	541	9 ADY21360	ADY21360 Murine no
2	993.5	35.0	542	9 ADZ22153	ADZ22153 Snow moun
3	990	34.9	535	4 AAB49707	AAB49707 Small rou
4	980.5	34.5	539	4 AAB49704	AAB49704 Small rou
5	980.5	34.5	544	4 AAB49703	AAB49703 Small rou
6	968.5	34.1	542	4 AAB49708	AAB49708 Small rou
7	967.5	34.1	546	4 AAB49702	AAB49702 Small rou
8	963.5	33.9	540	4 AAB49706	AAB49706 Small rou
9	962.5	33.9	530	4 AAB49701	AAB49701 Small rou
10	962.5	33.9	530	9 ADZ22152	ADZ22152 Normal v
11	958.5	33.8	530	9 AAR50972	AAR50972 Normal v
12	958.5	33.8	530	7 ADC72176	ADC72176 Normal v
13	958.5	33.8	530	7 ADB63372	ADB63372 Normal v
14	958.5	33.8	530	9 ADZ22151	ADZ22151 Normal v
15	958.5	33.8	530	9 ADZ22919	ADZ22919 Plant-opt
16	958.5	33.8	530	9 ADZ22920	ADZ22920 Normal v
17	958.5	33.8	530	9 ADZ22915	ADZ22915 Normal v
18	951	33.5	545	4 AAB49700	AAB49700 Small rou
19	936.5	33.0	548	4 AAB49705	AAB49705 Small rou
20	934.5	32.9	530	2 AAR50991	AAR50991 Small rou
21	923.5	32.5	548	5 AAU91272	AAU91272 Normal v
22	923.5	32.5	550	4 AAB49709	AAB49709 Small rou
23	837	29.5	541	4 AAB49710	AAB49710 Small rou
24	303.5	10.7	579	2 AAM08143	AAM08143 RHDV caps

25	260.5	9.2	669	4 AAB67461	AAB67461 Amino aci
26	252	8.9	547	4 AAB67462	AAB67462 Amino aci
27	249	8.8	668	4 AAM50108	AAM50108 Feline ca
28	249	8.8	671	4 AAM50107	AAM50107 Feline ca
29	249	8.8	671	8 AD574102	AD574102 Feline ca
30	248	8.7	668	8 AD574103	AD574103 Virulent
31	247.5	8.7	667	8 AD574104	AD574104 Virulent
32	247.5	8.7	668	8 AD574105	AD574105 Virulent
33	244	8.6	623	4 AAB47044	AAB47044 Feline ca
34	244	8.6	623	4 AAB47043	AAB47043 Feline ca
35	241	8.5	668	2 AAR10686	AAR10686 Feline ca
36	241	8.5	668	4 AAB04304	AAB04304 Feline ca
37	233	8.2	622	4 AAB47045	AAB47045 Feline ca
38	138	4.9	40	5 AAU91273	AAU91273 Normal v
39	123	4.3	40	5 AAU91274	AAU91274 Normal v
40	118.5	4.2	736	6 ADY73734	ADY73734 Foot-and-
41	118.5	4.2	1698	6 ABO14663	ABO14663 Novel hum
42	116.5	4.1	1147	5 AAB76724	AB76724 Foot and
43	115.5	4.1	511	4 AAB19847	AAB19847 Mycobacte
44	115.5	4.1	511	5 ABO05990	ABO05990 M. tuberc
45	115.5	4.1	934	1 AAP20016	AAP20016 Sequence

ALIGNMENTS

RESULT 1	ADY21360	ADY21360 standard; protein; 541 AA.
XX	ADY21360	
AC	ADY21360	
XX	ADY21360	
DT	05-MAY-2005	(First entry)
XX		
DB	Murine norovirus 1 (NMV-1) consensus DNA ORF2 protein.	
XX		
KW	Diagnosis; enteritis; antiinflammatory; gastrointestinal-gen.;	
KW	Gastroenteritis; gastrointestinal disease; inflammation; virulence;	
KW	Vaccine; animal disease model.	
XX		
OS	Murine norovirus 1.	
XX		
PH	Key	Location/Qualifiers
FT	Misc-difference 32	/note= "Xaa equals variable amino acid"
FT	Misc-difference 52	/note= "Xaa equals variable amino acid"
FT	Misc-difference 106	/note= "Xaa equals variable amino acid"
FT	Misc-difference 291	/note= "Xaa equals variable amino acid"
FT	Misc-difference 291	/note= "Xaa equals variable amino acid"
XX		
PN	US2005037016-A1.	
XX		
PD	17-FEB-2005.	
XX		
PF	14-JAN-2004; 2004US-00757832.	
XX		
PR	14-JAN-2003; 2003US-0440016P.	
XX		
PA	(VIRG/) VIRGIN H W.	
XX		
PI	Virgin HW;	
XX		
DR	WPI, 2005-161903/17.	
XX		
DR	N-PSDB; ADY21358.	
XX		
PT	New isolated polynucleotide encoding murine norovirus-1 (NMV-1) useful	
PT	for treating and/or preventing non-bacterial epidemic gastroenteritis	
PT	caused by murine noroviruses.	
XX		
PS	Claim 12; SEQ ID NO 3; 42bp; English.	
XX		

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

M protein - protein search, using SW model

on on: December 16, 2005, 14:18:50 / Search time 1.57709 Seconds
(without alignments)
888.505 Million cell updates/sec

file: US-10-757-832-4

effect score: 1066
sequence: 1 MAGALFAGIGGLMIGINS.....OGTYNGRFVSLPKIGSSRA 208

oring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

searched: 51470 seqs, 6736768 residues

total number of hits satisfying chosen parameters: 51470

inimum DB seq length: 0
aximum DB seq length: 200000000

ost-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

atabase : Published Applications_AA_New:

- 1: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US11_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	88.5	8.3	371	7	US-11-137-671-16
2	86.5	8.1	1263	7	US-11-076-163-3
3	83.5	7.8	1170	7	US-11-080-026-2
4	82.5	7.7	1255	7	US-11-022-562-235
5	81.5	7.6	758	6	US-10-485-517-144
6	80	7.5	406	6	US-10-821-234-1026
7	79	7.4	432	6	US-10-878-556A-72
8	78.5	7.4	394	6	US-10-467-657-4698
9	77.5	7.3	669	6	US-10-878-556A-87
10	77.5	7.3	757	7	US-11-110-082-35
11	76.5	7.2	781	7	US-11-194-246-344
12	76.5	7.2	1970	6	US-10-821-234-1641
13	75.5	7.1	451	6	US-10-995-561-886
14	74.5	7.0	463	6	US-10-793-626-960
15	74.5	7.0	1463	6	US-10-971-982-3
16	74	6.9	612	6	US-10-467-657-3988
17	74	6.9	859	7	US-11-188-743-16
18	73.5	6.9	358	6	US-10-995-561-885
19	73.5	6.9	358	6	US-10-995-561-885
20	73.5	6.9	388	6	US-10-995-561-889
21	73.5	6.9	405	7	US-11-083-551A-29
22	73.5	6.9	405	7	US-11-083-551A-29
23	73.5	6.9	405	7	US-11-083-551A-50
24	73.5	6.9	473	6	US-10-793-626-548
25	73.5	6.9	1304	6	US-10-821-234-1648

26	72.5	6.8	761	7	US-11-110-082-34	Sequence 34, Appl
27	72	6.8	654	7	US-11-110-082-24	Sequence 24, Appl
28	72	6.8	3655	7	US-11-075-185-5	Sequence 5, Appl
29	71.5	6.7	509	6	US-10-821-234-1093	Sequence 1093, Ap
30	71	6.7	405	6	US-10-821-234-1357	Sequence 1357, Ap
31	70.5	6.6	416	6	US-10-793-626-2	Sequence 2, Appl
32	70.5	6.6	5024	6	US-10-793-626-2964	Sequence 2964, Ap
33	70	6.6	2504	6	US-10-647-956A-8	Sequence 8, Appl
34	69.5	6.5	268	6	US-10-510-386-180	Sequence 180, App
35	69.5	6.5	972	6	US-10-821-234-1587	Sequence 1587, Ap
36	69.5	6.5	1404	6	US-10-878-556A-169	Sequence 169, App
37	69	6.5	438	6	US-10-995-561-589	Sequence 589, App
38	69	6.5	477	6	US-10-995-561-587	Sequence 587, App
39	69	6.5	477	6	US-10-995-561-588	Sequence 588, App
40	69	6.5	2516	6	US-10-647-956A-2	Sequence 2, Appl
41	68.5	6.4	249	7	US-11-054-515-2049	Sequence 2049, Ap
42	68.5	6.4	894	6	US-10-485-517-416	Sequence 416, App
43	68.5	6.4	1290	6	US-10-485-517-141	Sequence 141, App
44	68	6.4	251	7	US-11-054-515-1812	Sequence 1812, Ap
45	68	6.4	481	7	US-11-116-939-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-11-137-671-16
Sequence 16, Application US/11137671
Publication No. US20050268350A1
GENERAL INFORMATION:
APPLICANT: Kirschbaum, Bernd
Berglund, Erick
Meisterernst, Michael
Polites, Greg
TITLE OF INVENTION: PURIFICATION OF HIGHER ORDER TRANSCRIPTION
COMPLEXES FROM TRANSGENIC
NON-HUMAN ANIMALS
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESSES:
ADDRESSER: HELLER, EHRMAN, WHITE & MCANULTY
STREET: 1666 K Street, N.W., Suite 300
CITY: Washington
STATE: D.C.
COUNTRY: USA
ZIP: 20006
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/11137, 671
FILING DATE: 25-May-2005
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/849, 243
FILING DATE: 07-May-2001
ATTORNEY/AGENT INFORMATION:
NAME: Granados, Patricia D.
REGISTRATION NUMBER: 33,683
REFERENCE/DOCKET NUMBER: 38005-0148
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)912-2020
TELEFAX: (202)912-2020
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 371 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULAR TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 16:
US-11-137-671-16
Query Match 8.3%; Score 88.5; DB 7; Length 371.

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OW protein - protein search, using sw model

Run on: December 16, 2005, 14:13:00 ; Search time 25.234 Seconds
(without alignments)
3444.190 Million cell updates/sec

Title: US-10-757-832-4

Perfect score: 1066
Sequence: 1 MAGALFGAIGGIMGIIGNS.....OGTYTNGRVSLPKIGSSRA 208

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications AA Main:*
1: /cgn2_6/prodata/1/pubppaa/US07_PUBCOMB.pep:*
2: /cgn2_6/prodata/1/pubppaa/US08_PUBCOMB.pep:*
3: /cgn2_6/prodata/1/pubppaa/US09_PUBCOMB.pep:*
4: /cgn2_6/prodata/1/pubppaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/prodata/1/pubppaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/prodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1066	100.0	208	US-10-757-832-4	Sequence 4, Appl1
2	188	17.6	212	US-10-314-739-4	Sequence 4, Appl1
3	106.5	10.0	825	US-10-369-493-22501	Sequence 22501, A
4	104	9.8	2703	US-11-097-143-7590	Sequence 7590, A
5	103	9.7	494	US-09-833-790-234	Sequence 234, App
6	100	9.4	475	US-10-450-763-40845	Sequence 40845, A
7	97.5	9.1	1032	US-09-733-643-16	Sequence 16, Appl1
8	97.5	9.1	1032	US-10-120-801-64	Sequence 64, Appl1
9	97	9.1	551	US-10-437-963-152729	Sequence 152729, A
10	97	9.1	3828	US-10-732-823-15040	Sequence 15040, A
11	96.5	9.1	1146	US-10-437-963-110893	Sequence 110893, A
12	96.5	9.1	4823	US-10-051-874-169	Sequence 169, App
13	96	9.0	511	US-10-451-467A-468	Sequence 468, App
14	95.5	9.0	305	US-10-372-054-18	Sequence 18, Appl1
15	95.5	9.0	1013	US-11-097-143-39909	Sequence 39909, A
16	94.5	8.9	547	US-11-097-143-13383	Sequence 13383, A
17	93.5	8.8	748	US-10-437-963-125846	Sequence 125846, A
18	93.5	8.8	828	US-11-097-143-24114	Sequence 24114, A
19	93	8.7	413	US-10-424-599-240403	Sequence 240403, A
20	92	8.6	575	US-11-097-143-17316	Sequence 17316, A
21	92	8.6	584	US-10-382-122A-47689	Sequence 47689, A
22	92	8.6	1237	US-10-335-977-5116	Sequence 5116, App
23	91	8.5	183	US-10-424-599-194937	Sequence 194937, A
24	91	8.5	1112	US-10-450-763-52772	Sequence 52772, A
25	90	8.4	207	US-10-424-599-204198	Sequence 204198, A
26	90	8.4	347	US-10-282-122A-49941	Sequence 49941, A
27	89.5	8.4	355	US-10-425-115-342321	Sequence 342321, A

28	89.5	8.4	576	US-10-425-114-42381	Sequence 42381, A
29	89	8.3	560	US-10-425-115-306352	Sequence 306352, A
30	89	8.3	603	US-10-425-114-42780	Sequence 42780, A
31	89	8.3	975	US-11-097-143-8637	Sequence 8637, App
32	89	8.3	1448	US-10-408-765A-998	Sequence 998, App
33	88.5	8.3	338	US-09-933-638A-12	Sequence 12, Appl1
34	88.5	8.3	339	US-10-116-275-184	Sequence 184, App
35	88.5	8.3	339	US-10-818-694-2	Sequence 2, Appl1
36	88.5	8.3	345	US-10-818-694-15	Sequence 15, Appl1
37	88.5	8.3	371	US-09-849-243-16	Sequence 16, Appl1
38	88.5	8.3	468	US-10-739-930-8257	Sequence 8257, App
39	88.5	8.3	481	US-10-233-584A-3	Sequence 3, Appl1
40	88.5	8.3	641	US-10-233-584A-1	Sequence 1, Appl1
41	88.5	8.3	643	US-09-801-368-236	Sequence 236, App
42	88	8.3	318	US-10-351-891-126	Sequence 126, App
43	88	8.3	318	US-10-699-113-31	Sequence 31, Appl1
44	88	8.3	339	US-10-282-122A-45100	Sequence 45100, A
45	88	8.3	577	US-10-425-115-329192	Sequence 329192, A

ALIGNMENTS

```

RESULT 1
US-10-757-832-4
; Sequence 4, Application US/10757832
; Publication No. US20050037016A1
; GENERAL INFORMATION:
; APPLICANT: VIRGIN, HERBERT W.
; TITLE OF INVENTION: MURINE CALICIVIRUS
; FILE REFERENCE: 56029-45752
; CURRENT APPLICATION NUMBER: US/10/757,832
; PRIOR FILING DATE: 2004-01-14
; PRIOR APPLICATION NUMBER: 60/440,016
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 4
; LENGTH: 208
; TYPE: PRT
; ORGANISM: Murine Norovirus type 1
US-10-757-832-4

Query Match      100.0%; Score 1066; DB 5; Length 208;
Best Local Similarity 100.0%; Pred. No. 2.1e-94;
Matches 208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAGALFGAIGGIMGIIGNSIVNOLANKOLAAQFGNSSLATOIOAQKDLTLMGQ 60
DB 1 MAGALFGAIGGIMGIIGNSIVNOLANKOLAAQFGNSSLATOIOAQKDLTLMGQ 60
QY 61 OFNOQLQINSFKHDEMLGAQVOAQAQOENMINITAOLOAAGFRTATRLAQQOPT 120
DB 61 OFNOQLQINSFKHDEMLGAQVOAQAQOENMINITAOLOAAGFRTATRLAQQOPT 120
QY 121 RAVDSGRTYTNANDPVTPGSGFTYTTTPGQVTSRPVDTSLPLISGRLPBLRGSSWS 180
DB 121 RAVDSGRTYTNANDPVTPGSGFTYTTTPGQVTSRPVDTSLPLISGRLPBLRGSSWS 180
QY 181 PRDHPATOGTYTNGRVSLPKIGSSRA 208
DB 181 PRDHPATOGTYTNGRVSLPKIGSSRA 208

RESULT 2
US-10-314-739-4
; Sequence 4, Application US/10314739
; Publication No. US20030129586A1
; GENERAL INFORMATION:
; APPLICANT: Estes, Mary K
; Jjiang, Xi
; Graham, David Y
; TITLE OF INVENTION: Methods and Reagents to Detect and

```

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using SW model

Run on: December 16, 2005, 14:12:48 ; Search time 7.71019 Seconds
(without alignments)
2230.364 Million cell updates/sec

Title: US-10-757-832-4

Perfect score: 1066
Sequence: 1 MAGALFGAIGGGLMGIIGNS.....OGTYNGRPVSLPRIGSSRA 208

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database:

Issued Patents AA:
1: /cgn2_6/ptodata/1/1aa/5.COMB.pdp:*
2: /cgn2_6/ptodata/1/1aa/6.COMB.pdp:*
3: /cgn2_6/ptodata/1/1aa/H.COMB.pdp:*
4: /cgn2_6/ptodata/1/1aa/PCITUS.COMB.pdp:*
5: /cgn2_6/ptodata/1/1aa/RE.COMB.pdp:*
6: /cgn2_6/ptodata/1/1aa/backfile1.pdp:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	188	17.6	212	US-08-486-049-4	Sequence 4, Appli
2	188	17.6	212	US-10-314-739A-4	Sequence 4, Appli
3	169.5	15.9	170	US-10-314-739A-6	Sequence 6, Appli
4	104	9.8	2703	US-08-185-432-19	Sequence 19, Appli
5	104	9.8	2703	US-08-899-232-4	Sequence 4, Appli
6	104	9.8	2703	US-09-121-457-4	Sequence 4, Appli
7	97.5	9.1	1032	US-09-733-643B-16	Sequence 16, Appli
8	95.5	9.0	305	US-09-339-159B-18	Sequence 18, Appli
9	89.5	8.4	624	US-08-947-965-78	Sequence 27, Appli
10	89.5	8.4	655	US-08-469-202-27	Sequence 28, Appli
11	89.5	8.4	655	US-08-469-202-28	Sequence 34, Appli
12	89.5	8.4	655	US-08-484-434C-34	Sequence 35, Appli
13	89.5	8.4	655	US-08-484-434C-35	Sequence 35, Appli
14	89.5	8.4	655	US-09-384-361-34	Sequence 35, Appli
15	89.5	8.4	655	US-09-384-361-35	Sequence 35, Appli
16	89	8.3	1108	US-09-538-092-29	Sequence 29, Appli
17	88.5	8.3	339	US-09-324-258-2	Sequence 2, Appli
18	88.5	8.3	339	US-09-538-092-964	Sequence 964, App
19	88.5	8.3	343	US-09-324-258-15	Sequence 15, Appli
20	88.5	8.3	643	US-09-196-270-3	Sequence 3, Appli
21	88.5	8.3	643	US-09-487-558B-236	Sequence 236, App
22	88	8.3	354	US-09-328-352-7262	Sequence 7262, Ap
23	86.5	8.1	732	US-09-270-016-11696	Sequence 11696, A
24	86.5	8.1	1463	US-09-949-016-11696	Sequence 2, Appli
25	86.5	8.1	1464	US-08-891-640-2	Sequence 6738, Ap
26	86.5	8.1	1464	US-09-949-016-6738	Sequence 2, Appli
27	86.5	8.1	1464	US-09-842-256-2	Sequence 2, Appli

28	84.5	7.9	390	US-09-252-991A-17829	Sequence 17829, A
29	84.5	7.9	793	US-09-568-256-10	Sequence 10, Appli
30	84	7.9	314	US-09-328-352-4934	Sequence 4934, Ap
31	83.5	7.8	150	US-09-647-140B-23	Sequence 23, Appli
32	83.5	7.8	194	US-09-270-767-60105	Sequence 60105, A
33	83.5	7.8	589	US-10-261-164-2	Sequence 2, Appli
34	83.5	7.8	966	US-09-487-558B-372	Sequence 372, App
35	83.5	7.8	1065	US-08-630-172-9	Sequence 9, Appli
36	83.5	7.8	1065	US-09-375-419-9	Sequence 9, Appli
37	83.5	7.8	1170	US-08-789-078-2	Sequence 2, Appli
38	83.5	7.8	1170	US-08-752-633-2	Sequence 2, Appli
39	83.5	7.8	1170	US-10-261-164-1	Sequence 1, Appli
40	83.5	7.8	1170	PCT-US95-04886-2	Sequence 2, Appli
41	83	7.8	263	US-09-248-796A-23610	Sequence 23610, A
42	83	7.8	385	US-09-328-352-4372	Sequence 4372, Ap
43	83	7.8	675	US-09-248-796A-20699	Sequence 20699, A
44	83	7.8	801	US-09-351-150A-25	Sequence 25, Appli
45	83	7.8	865	US-09-902-540-10416	Sequence 10416, A

ALIGNMENTS

RESULT 1
US-08-486-049-4
Sequence 4, Application US/08486049
Patent No. 6572862
GENERAL INFORMATION:
APPLICANT: Bates, Mary K
APPLICANT: Jiang, Xi
TITLE OF INVENTION: Methods and Reagents to Detect and
TITLE OF INVENTION: Characterize No. 6572862walk and Related Viruses
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESSES:
ADDRESS: Fulbright & Jaworski L.L.P.
STREET: 801 Pennsylvania Ave., N.W.
CITY: Washington, D.C.
STATE:
COUNTRY: USA
ZIP: 20004
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/486,049
FILING DATE: June 7, 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Davis, Peter
REGISTRATION NUMBER: 36,119
REFERENCE/DOCKET NUMBER: 311,023
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-662-0200
TELEFAX: 202-662-4643
TELEX:
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 212 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-486-049-4
Query Match 17.6%; Score 188; DB-2; Length 212;
Best local similarity 31.7%; Pred. No. 4.1e-12;
Matches 60; Conservative 15; Mismatches 70; Indels 44; Gaps 6;
DB 1 MAGALFGAIGGGLMGIIGNSISNVONTQANKQLAAGQFGNSLLATQIQAKQKLTLMQGO 60
SALGAGCIQVCGEALASQ 33

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using BW model

Run on: December 16, 2005, 13:39:53 / Search time 35.0463 Seconds
(without alignments)
4187.310 Million cell updates/sec

Title: US-10-757-832-4
Perfect score: 1066
Sequence: 1 MAGALFAGIGGIMGIGNS.....GGTYNGRFPVSLPIGSSRA 208

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database: UniProt 05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1066	100.0	208	Q80J93_9CALI	Q80J93 murine novo
2	255.5	24.0	219	Q91164_9CALI	Q91164 human calic
3	254	23.8	258	Q917W7_9CALI	Q917W7 norwalk-11k
4	251	23.5	258	Q917X0_9CALI	Q917X0 norwalk-11k
5	248.5	23.3	257	Q918A9_9CALI	Q918A9 norwalk-11k
6	248.5	23.3	258	Q5F4T4_9CALI	Q5F4T4 norwalk-11k
7	247	23.2	259	Q80RDS_9CALI	Q80RDS snow mounta
8	246.5	23.1	257	Q91H08_9CALI	Q91H08 human calic
9	242.5	22.7	259	Q80X17_9CALI	Q80X17 norwalk-11k
10	242.5	22.7	259	Q80V780_9CALI	Q80V780 norwalk-11k
11	241.5	22.7	259	Q66294_9CALI	Q66294 human calic
12	240.5	22.6	258	Q6XDL3_9CALI	Q6XDL3 human calic
13	239.5	22.5	262	Q917M4_9CALI	Q917M4 norwalk-11k
14	238.5	22.4	242	Q917V5_9CALI	Q917V5 norwalk-11k
15	238	22.3	259	Q783X9_9CALI	Q783X9 norwalk-11k
16	238	22.3	259	Q80V783_9CALI	Q80V783 norwalk-11k
17	237.5	22.3	259	Q918B2_9CALI	Q918B2 norwalk-11k
18	236.5	22.2	268	Q91322_9CALI	Q91322 human calic
19	235.5	22.1	259	Q54AD5_9CALI	Q54AD5 human calic
20	235.5	22.1	268	Q6REW0_9CALI	Q6REW0 norwalk-11k
21	235.5	22.1	268	Q917W1_9CALI	Q917W1 norwalk-11k
22	233.5	21.9	242	Q917V8_9CALI	Q917V8 norwalk-11k
23	233.5	21.9	259	Q783X5_9CALI	Q783X5 norwalk-11k
24	233.5	21.9	259	Q80V777_9CALI	Q80V777 norwalk-11k
25	232.5	21.8	268	Q5XKX0_9CALI	Q5XKX0 norwalk-11k
26	232	21.8	216	Q78K9_9CALI	Q78K9 bovine ente
27	232	21.8	282	Q78BL0_9CALI	Q78BL0 bovine ente
28	231.5	21.7	258	Q918A6_9CALI	Q918A6 norwalk-11k
29	231.5	21.7	268	Q68538_9CALI	Q68538 norwalk-11k
30	231.5	21.7	268	Q68P17_9CALI	Q68P17 norwalk-11k
31	231.5	21.7	268	Q77080_9CALI	Q77080 canberwell

32	231.5	21.7	282	Q8B4Y8_9CALI	Q8B4Y8 norwalk-11k
33	230.5	21.6	268	Q6PPJ0_9CALI	Q6PPJ0 norwalk-11k
34	230.5	21.6	268	Q6PPJ3_9CALI	Q6PPJ3 norwalk-11k
35	230.5	21.6	268	Q6PPJ6_9CALI	Q6PPJ6 norwalk-11k
36	230.5	21.6	268	Q6PPJ9_9CALI	Q6PPJ9 norwalk-11k
37	230.5	21.6	268	Q6PPK2_9CALI	Q6PPK2 norwalk-11k
38	230.5	21.6	268	Q6PPK5_9CALI	Q6PPK5 norwalk-11k
39	230.5	21.6	268	Q6PPK8_9CALI	Q6PPK8 norwalk-11k
40	230.5	21.6	268	Q6PPL1_9CALI	Q6PPL1 norwalk-11k
41	230.5	21.6	268	Q6PPL4_9CALI	Q6PPL4 norwalk-11k
42	230.5	21.6	268	Q6PPL7_9CALI	Q6PPL7 norwalk-11k
43	230.5	21.6	268	Q6PPM0_9CALI	Q6PPM0 norwalk-11k
44	230.5	21.6	268	Q6PPM3_9CALI	Q6PPM3 norwalk-11k
45	230.5	21.6	268	Q6PPM6_9CALI	Q6PPM6 norwalk-11k

ALIGNMENTS

RESULT 1	Q80J93_9CALI	PRELIMINARY;	PRT;	208 AA.
ID	Q80J93_9CALI	PRELIMINARY;	PRT;	208 AA.
AC	Q80J93_9CALI	PRELIMINARY;	PRT;	208 AA.
DT	01-JUN-2003 (TREMBLrel. 24, Created)			
DT	01-JUN-2003 (TREMBLrel. 24, Last sequence update)			
DT	01-OCT-2003 (TREMBLrel. 25, Last annotation update)			
DE	Small basic protein.			
OS	Murine norovirus 1.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;			
OX	Norovirus.			
RN	NCBI_Taxid-223997;			
RP	NUCLEOTIDE SEQUENCE.			
RX	MEDLINE=22511930; PubMed=12624267; DOI=10.1126/science.1077905;			
RA	Karet S.M., Webus C.B., Lay M., Davidson J., Virgin H.W.;			
RT	"STAT1-dependent innate immunity to a Norwalk-like virus.";			
RL	Science 299:1575-1578 (2003).			
DR	EMBL; AY228235; AA063100.1; -; Genomic_RNA.			
DR	InterPro; IPR004278; RNA_capsid.			
DR	Pfam; PF03035; RNA_capsid; 1.			
SQ	SEQUENCE 208 AA; 22073 MW; 9A33B823C665C01P CRC64;			
Query Match	100.0%; Score 1066; DB 2; Length 208;			
Best Local Similarity	100.0%; Pred. No. 2.8e-78;			
Matches	208; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	1 MAGALFAGIGGIMGIGNSISNVONTQANKQLAAQEGYNSSLATQIAQKDLTMQ 60			
DB	1 MAGALFAGIGGIMGIGNSISNVONTQANKQLAAQEGYNSSLATQIAQKDLTMQ 60			
QY	61 QPNQQLQNSFKHLEMLGAQVQAQAQENANIKTAQOLAAGSKTDATRLALGQPT 120			
DB	61 QPNQQLQNSFKHLEMLGAQVQAQAQENANIKTAQOLAAGSKTDATRLALGQPT 120			
QY	121 RAVDMSGRYYTANQPVYGFSGFTPTTPGQVTSRPVDSPLPSGRLPLSGSWS 180			
DB	121 RAVDMSGRYYTANQPVYGFSGFTPTTPGQVTSRPVDSPLPSGRLPLSGSWS 180			
QY	181 PRDHTPATGGTYNGRFPVSLPIGSSRA 208			
DB	181 PRDHTPATGGTYNGRFPVSLPIGSSRA 208			
RESULT 2	Q91164_9CALI	PRELIMINARY;	PRT;	219 AA.
ID	Q91164_9CALI	PRELIMINARY;	PRT;	219 AA.
AC	Q91164_9CALI	PRELIMINARY;	PRT;	219 AA.
DT	01-DEC-2001 (TREMBLrel. 19, Created)			
DT	01-DEC-2001 (TREMBLrel. 19, Last sequence update)			
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)			
DR	Minor structural protein.			
OS	Human calicivirus NVV/MOH/99.			
OC	Viruses; ssRNA positive-strand viruses, no DNA stage; Caliciviridae;			

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: December 16, 2005, 13:39:38 / Search time 30.5779 seconds
(without alignments)
2988.783 Million cell updates/sec

Title: US-10-757-832-4

Perfect score: 1066
Sequence: 1 MAGALFGAIGGIMGIGNS.....OGTYNGRFLSLKIGSRA 208

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

A_Geneseq_21.*
1: geneseqp19808:*
2: geneseqp19908:*
3: geneseqp20008:*
4: geneseqp20018:*
5: geneseqp20028:*
6: geneseqp20038:*
7: geneseqp20038:*
8: geneseqp20048:*
9: geneseqp20058:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1066	100.0	208	9	ADY21361 Murine no
2	188	17.6	212	2	AAK50973 Norwalk v
3	188	17.6	212	7	ADCT2177 Norwalk v
4	188	17.6	212	7	ADBS6373 Norwalk v
5	169.5	15.9	170	7	ADCT2179 Norwalk v
6	169.5	15.9	170	7	ADL02214 Protein e
7	162.5	15.2	170	2	AAAT2299
8	106.5	10.0	825	8	ADBS44071 Bacteri
9	104	9.8	2703	4	ABBS0266 Drosophi
10	104	9.8	2703	8	ADL26916 Drosophi
11	103	9.7	293	4	ADM19740 Protein e
12	103	9.7	494	5	AAU69408 Lung sm
13	103	9.7	525	2	ADCS5533 Brono RNA
14	100	9.4	475	4	ABG10486 Novel hum
15	97.5	9.1	601	7	ADG39832 Protein s
16	97	9.1	484	4	AAW93708 Human pol
17	97	9.1	484	8	ADL1610 Human pro
18	97	9.1	528	7	ABM87141 Rice abio
19	97	9.1	1081	6	ABRS3539 Protein e
20	97	9.1	1081	7	ADK64412 Disease t
21	96.5	9.1	1337	3	AAAB12877 Murine JN
22	96.5	9.1	1337	3	AAAB12877 Murine JN
23	96	9.0	511	5	ABG93255 C. albica
24	95.5	9.0	305	3	AAAY54130 Amino aci

25	95.5	9.0	1013	4	ABB71039 Drosophi
26	94.5	8.9	547	4	ABB62197 Drosophi
27	93.5	8.8	828	4	ABB65774 Drosophi
28	92.5	8.7	1305	3	ABH12875 Murine JN
29	92	8.6	575	4	ABB63508 Drosophi
30	92	8.6	584	6	ABU19765 Protein e
31	92	8.6	1237	2	AAW55640 H. pylori
32	92	8.6	1237	2	AAV17187 H. pylori
33	92	8.6	1237	4	ABR91385 Microbial
34	91	8.5	1112	4	ABG22413 Novel hum
35	90	8.4	347	6	ABU22017 Protein e
36	90	8.4	1098	8	ABO52965 Human epi
37	90	8.4	1098	8	AD182501 Human mod
38	90	8.4	1336	3	AAH12878 Murine JN
39	89.5	8.4	576	8	ADK73015 Plant ful
40	89.5	8.4	655	2	AAK20139 Sequence
41	89.5	8.4	655	6	ABU62572 Cyclohex
42	89.5	8.4	655	6	ABU62573 Cyclohex
43	89.5	8.4	655	9	ADW42705 Klebstei
44	89.5	8.4	715	2	AAK20138 Sequence
45	89	8.3	603	8	ADK73414 Plant ful

ALIGNMENTS

Result 1	ADY21361	ADY21361 standard; protein; 208 AA.
XX	AC	ADY21361;
XX	DT	05-MAY-2005 (first entry)
DE	XX	Murine norovirus 1 (MNV-1) consensus DNA ORF3 protein.
KW	XX	Diagnosis; enteritis; anti-inflammatory; gastrointestinal-gen.;
KW	XX	gastroenteritis; gastrointestinal disease; inflammation; virocid;
KW	XX	vaccine; animal disease model.
OS	XX	Murine norovirus 1.
PN	XX	US2005037016-A1.
PD	XX	17-FEB-2005.
PF	XX	14-JAN-2004; 2004US-00757832.
PR	XX	14-JAN-2003; 2003US-0440016P.
PA	XX	(VIRG/) VIRGIN H W.
PI	XX	Virgin HW;
DR	XX	WPI; 2005-161903/17.
DR	XX	N-PSDB; ADY21358.
PT	XX	New isolated polynucleotide encoding murine norovirus-1 (MNV-1) useful
PT	XX	for treating and/or preventing non-bacterial epidemic gastroenteritis
PT	XX	caused by murine noroviruses.
PS	XX	Claim 15; SEQ ID NO 4; 42pp; English.
CC	XX	The present invention relates to a murine norovirus 1 (MNV-1) polypeptide
CC	XX	and its encoding polynucleotide. The invention is useful for the
CC	XX	treatment and prevention of non-bacterial epidemic gastroenteritis caused
CC	XX	by murine noroviruses. The present sequence is the murine norovirus 1
CC	XX	consensus DNA ORF3 (open reading frame) protein.
SQ	XX	Sequence 208 AA;
Query Match	100.0%;	Score 1066; DB 9; Length 208;
Best Local Similarity	100.0%;	Pred. No. 2.3e-98;